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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/129,758

DATE: 03/15/1999  
TIME: 08:37:47

Input Set: I129758.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

*see p. 5*

ENTERED

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1  <110> APPLICANT: Waldmann, Rainer
2  <120> TITLE OF INVENTION: MAMMAL NEURONAL ACID SENSING CATIONIC
3      CHANNEL, CLONING AND APPLICATIONS THEREOF
4  <130> FILE REFERENCE: 989.6701P
5  <140> CURRENT APPLICATION NUMBER: US/09/129,758
6  <141> CURRENT FILING DATE: 1998-08-05
7  <150> EARLIER APPLICATION NUMBER: PCT/FR98/00270
8  <151> EARLIER FILING DATE: 1998-02-11
9  <150> EARLIER APPLICATION NUMBER: FR 97/01574
10 <151> EARLIER FILING DATE: 1997-02-11
11 <150> EARLIER APPLICATION NUMBER: FR 97/09587
12 <151> EARLIER FILING DATE: 1997-07-28
13 <160> NUMBER OF SEQ ID NOS: 18
14 <170> SOFTWARE: PatentIn Ver. 2.0
15 <210> SEQ ID NO 1
16 <211> LENGTH: 3562
17 <212> TYPE: DNA
18 <213> ORGANISM: rat
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21 <222> LOCATION: (123)..(1700)
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25      gg atg gaa ttg aag acc gag gag gag gag gtg ggt ggt gtc cag ccg 167
26      Met Glu Leu Lys Thr Glu Glu Glu Glu Val Gly Gly Val Gln Pro
27      1          5          10          15
28      gtg agc atc cag gct ttc gcc agc agc tcc acg ctg cat ggt ctt gcc 215
29      Val Ser Ile Gln Ala Phe Ala Ser Ser Ser Thr Leu His Gly Leu Ala
30      20          25          30
31      cac atc ttc tcc tat gag cgg ctg tct ctg aag cgg gca ctg tgg gcc 263
32      His Ile Phe Ser Tyr Glu Arg Leu Ser Leu Lys Arg Ala Leu Trp Ala
33      35          40          45
34      ctg tgc ttc ctg ggt tgc ctg gcc gtc ctg ctg tgt gtg tgc act gag 311
35      Leu Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val Cys Thr Glu
36      50          55          60
37      cgt gtg cag tac tac ttc tgc tat cac cac gtc acc aag ctt gac gaa 359
38      Arg Val Gln Tyr Tyr Phe Cys Tyr His His Val Thr Lys Leu Asp Glu
39      65          70          75
40      gtg gct gcc tcc cag ctc acc ttc cct gct gtc aca ctg tgc aat ctc 407
41      Val Ala Ala Ser Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn Leu
42      80          85          90          95
43      aat gag ttc cgc ttt agc caa gtc tcc aag aat gac ctg tac cat gct 455
44      Asn Glu Phe Arg Phe Ser Gln Val Ser Lys Asn Asp Leu Tyr His Ala

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46	ggg	gag	ctg	ctg	gcc	ctg	ctc	aac	aac	agg	tat	gag	atc	ccg	gac	aca	503
47	Gly	Glu	Leu	Leu	Ala	Leu	Leu	Asn	Asn	Arg	Tyr	Glu	Ile	Pro	Asp	Thr	
48				115				120				125					
49	cag	atg	gct	gat	gaa	aag	cag	cta	gag	ata	ttg	cag	gac	aag	gcc	aac	551
50	Gln	Met	Ala	Asp	Glu	Lys	Gln	Leu	Glu	Ile	Leu	Gln	Asp	Lys	Ala	Asn	
51				130				135				140					
52	ttc	cgg	agc	ttc	aag	ccc	aag	ccc	ttc	aac	atg	cgt	gaa	ttc	tac	gac	599
53	Phe	Arg	Ser	Phe	Lys	Pro	Lys	Pro	Phe	Asn	Met	Arg	Glu	Phe	Tyr	Asp	
54				145				150				155					
55	aga	gcg	ggg	cac	gat	att	cga	gac	atg	ctg	ctc	tcg	tgc	cac	ttc	cgt	647
56	Arg	Ala	Gly	His	Asp	Ile	Arg	Asp	Met	Leu	Leu	Ser	Cys	His	Phe	Arg	
57				160				165				170					
58	ggg	gag	gcc	tgc	agc	gct	gaa	gat	ttc	aaa	gtg	gtc	ttc	act	cgg	tat	695
59	Gly	Glu	Ala	Cys	Ser	Ala	Glu	Asp	Phe	Lys	Val	Val	Phe	Thr	Arg	Tyr	
60				180				185				190					
61	ggg	aag	tgt	tac	aca	ttc	aac	tcg	ggc	caa	gat	ggg	cgg	cca	cgg	ctg	743
62	Gly	Lys	Cys	Tyr	Thr	Phe	Asn	Ser	Gly	Gln	Asp	Gly	Arg	Pro	Arg	Leu	
63				195				200				205					
64	aag	acc	atg	aaa	ggt	ggg	act	ggc	aat	ggc	ctg	gag	atc	atg	ctg	gac	791
65	Lys	Thr	Met	Lys	Gly	Gly	Thr	Gly	Asn	Gly	Leu	Glu	Ile	Met	Leu	Asp	
66				210				215				220					
67	att	cag	caa	gat	gaa	tat	ttg	cct	gtg	tgg	gga	gag	acc	gac	gag	aca	839
68	Ile	Gln	Gln	Asp	Glu	Tyr	Leu	Pro	Val	Trp	Gly	Glu	Thr	Asp	Glu	Thr	
69				225				230				235					
70	tcc	ttc	gaa	gca	ggc	atc	aaa	gtg	cag	atc	cac	agt	cag	gat	gaa	ccc	887
71	Ser	Phe	Glu	Ala	Gly	Ile	Lys	Val	Gln	Ile	His	Ser	Gln	Asp	Glu	Pro	
72				240				245				250					
73	cct	ttc	atc	gac	cag	ctg	ggc	ttt	ggt	gtg	gct	cca	ggt	ttc	cag	acg	935
74	Pro	Phe	Ile	Asp	Gln	Leu	Gly	Phe	Gly	Val	Ala	Pro	Gly	Phe	Gln	Thr	
75				260				265				270					
76	ttt	gtg	tct	tgc	cag	gag	cag	agg	ctc	atc	tac	ctg	ccc	tca	ccc	tgg	983
77	Phe	Val	Ser	Cys	Gln	Glu	Gln	Arg	Leu	Ile	Tyr	Leu	Pro	Ser	Pro	Trp	
78				275				280				285					
79	ggc	acc	tgc	aat	gct	gtt	acc	atg	gac	tcg	gat	ttc	ttc	gac	tcc	tac	1031
80	Gly	Thr	Cys	Asn	Ala	Val	Thr	Met	Asp	Ser	Asp	Phe	Phe	Asp	Ser	Tyr	
81				290				295				300					
82	agc	atc	act	gcc	tgc	cgg	att	gat	tgc	gag	acg	cgt	tac	ctg	gtg	gag	1079
83	Ser	Ile	Thr	Ala	Cys	Arg	Ile	Asp	Cys	Glu	Thr	Arg	Tyr	Leu	Val	Glu	
84				305				310				315					
85	aac	tgc	aac	tgc	cgt	atg	gtg	cac	atg	cca	ggg	gac	gcc	cca	tac	tgc	1127
86	Asn	Cys	Asn	Cys	Arg	Met	Val	His	Met	Pro	Gly	Asp	Ala	Pro	Tyr	Cys	
87				320				325				330					
88	act	cca	gag	cag	tac	aag	gag	tgt	gca	gat	cct	gcc	ctg	gac	ttc	cta	1175
89	Thr	Pro	Glu	Gln	Tyr	Lys	Glu	Cys	Ala	Asp	Pro	Ala	Leu	Asp	Phe	Leu	
90				340				345				350					
91	gtg	gag	aaa	gac	cag	gaa	tac	tgc	gtg	tgt	gag	atg	cct	tgc	aac	ctg	1223
92	Val	Glu	Lys	Asp	Gln	Glu	Tyr	Cys	Val	Cys	Glu	Met	Pro	Cys	Asn	Leu	
93				355				360				365					
94	acc	cgc	tac	ggc	aag	gag	ctg	tcc	atg	gtc	aag	atc	cca	agc	aaa	gcc	1271

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97	tcc gcc aag tac ctg gcc aag aag ttc aac aaa tcg gag cag tac ata	1319
98	Ser Ala Lys Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu Gln Tyr Ile	
99	385 390 395	
100	ggg gag aac att ctg gtg ctg gac att ttc ttt gaa gtc ctc aac tat	1367
101	Gly Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Val Leu Asn Tyr	
102	400 405 410 415	
103	gag acc atc gag cag aaa aag gcc tat gag atc gca ggg ctg ttg ggt	1415
104	Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly Leu Leu Gly	
105	420 425 430	
106	gac atc ggg ggc cag atg ggg ttg ttc atc ggt gcc agc atc ctc acc	1463
107	Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu Thr	
108	435 440 445	
109	gtg ctg gaa ctc ttt gac tat gcc tac gag gtc att aag cac agg ctg	1511
110	Val Leu Glu Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys His Arg Leu	
111	450 455 460	
112	tgc aga cgt gga aag tgc cag aag gag gct aag agg agc agc gca gac	1559
113	Cys Arg Arg Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser Ser Ala Asp	
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115	aag ggc gtg gcg ctc agc ctg gat gac gtc aaa aga cac aat ccc tgc	1607
116	Lys Gly Val Ala Leu Ser Leu Asp Asp Val Lys Arg His Asn Pro Cys	
117	480 485 490 495	
118	gag agc ctc cga gga cat cct gcc ggg atg acg tac gct gcc aac atc	1655
119	Glu Ser Leu Arg Gly His Pro Ala Gly Met Thr Tyr Ala Ala Asn Ile	
120	500 505 510	
121	cta cct cac cat ccc gct cga ggc acg ttt gag gac ttt acc tgc	1700
122	Leu Pro His His Pro Ala Arg Gly Thr Phe Glu Asp Phe Thr Cys	
123	515 520 525	
124	taagccctcg caggccgctg taccaaaggc ctagggtggg agggctggg gagcaagggg	1760
125	cccccaactg ccccagcta ccctgtggac ttaactgcat tcctggtcag tggttccctc	1820
126	ttgtctgtgg tgagaaagga gtcttgacca tagagtcctc tcccagcctc tatcccatct	1880
127	ttttatttta atttaatcac atttgctctg taatattgct tgaggctggg gatcgatgatt	1940
128	tccccccagt tcttttattg ttgagaatag ttttctctat tctgggtttt ctgttatttc	2000
129	aaatgaatct gcaaattgct cttcccatct ctatgaagaa ttgctgttga attttgatgg	2060
130	ggattgtatt gaatctgtag attgcctttg gtaagatggc catttttact atgttaatcc	2120
131	tgccaattca tgagcaagg agatctttct atctctgaaa tctacttcag tttctttctt	2180
132	cagagacttg aagttcttgt cataaaaaatc tttttgggta gagccacacc aaggtatttt	2240
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140	atgggccttg aattcctgat atttccaaga cttttaacat gaaggggttt tgaaatttgc	2720
141	caaagtcttt ctcagcatct aatgagatga tcatgtgccc tccccccacc ttgagtttgt	2780
142	ttatatagtg ggttacatga aaggatcatt tctaatagtc cacaagtctg ccaaactctg	2840
143	ctgattgtga ctcatctcca tagcaggctc tataacttct ctaacagatt gcattaaact	2900
144	ctgcttgggg aaggcattac ctcttggttg aagcaatggt gtagtttcta tgcctgctga	2960

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147      gctagagata ctccctcgaa ctgcaaaaga aatctcttgg ctaagcatat aatcaagcct 3140
148      cagggttttct ttttattaaa tagctgcttg taagaaagtg gacactaagc atatacctca 3200
149      aaggggagaca gaatgactct gtgccttcac tgatggaagt ctgggttaca aattacatca 3260
150      gaagaaccta tcatagttaa acatctcatt cccctggtat aatcccttct agaaatacac 3320
151      ttgtgactct gaaatgttat aatcgtgaca actaggctgt tacagatata ccaagttaaa 3380
152      tttgatagag aaaccaggct tggagcctca tgtccatagg gcaagaggaa gatgctgagt 3440
153      gttaaagggt ggtttgagcg aagaacaata ccttggtgtca caaaaatgaa aggaaaaaag 3500
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155      aa                                                                                      3562

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156 &lt;210&gt; SEQ ID NO 2

157 &lt;211&gt; LENGTH: 526

158 &lt;212&gt; TYPE: PRT

159 &lt;213&gt; ORGANISM: rat

160 &lt;400&gt; SEQUENCE: 2

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164      20          25          30
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166      35          40          45
167      Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val Cys Thr Glu Arg
168      50          55          60
169      Val Gln Tyr Tyr Phe Cys Tyr His His Val Thr Lys Leu Asp Glu Val
170      65          70          75          80
171      Ala Ala Ser Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn Leu Asn
172      85          90          95
173      Glu Phe Arg Phe Ser Gln Val Ser Lys Asn Asp Leu Tyr His Ala Gly
174      100         105         110
175      Glu Leu Leu Ala Leu Leu Asn Asn Arg Tyr Glu Ile Pro Asp Thr Gln
176      115         120         125
177      Met Ala Asp Glu Lys Gln Leu Glu Ile Leu Gln Asp Lys Ala Asn Phe
178      130         135         140
179      Arg Ser Phe Lys Pro Lys Pro Phe Asn Met Arg Glu Phe Tyr Asp Arg
180      145         150         155         160
181      Ala Gly His Asp Ile Arg Asp Met Leu Leu Ser Cys His Phe Arg Gly
182      165         170         175
183      Glu Ala Cys Ser Ala Glu Asp Phe Lys Val Val Phe Thr Arg Tyr Gly
184      180         185         190
185      Lys Cys Tyr Thr Phe Asn Ser Gly Gln Asp Gly Arg Pro Arg Leu Lys
186      195         200         205
187      Thr Met Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu Asp Ile
188      210         215         220
189      Gln Gln Asp Glu Tyr Leu Pro Val Trp Gly Glu Thr Asp Glu Thr Ser
190      225         230         235         240
191      Phe Glu Ala Gly Ile Lys Val Gln Ile His Ser Gln Asp Glu Pro Pro
192      245         250         255
193      Phe Ile Asp Gln Leu Gly Phe Gly Val Ala Pro Gly Phe Gln Thr Phe
194      260         265         270

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**RAW SEQUENCE LISTING**  
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198              290                      295                      300
199      Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr Leu Val Glu Asn
200      305                      310                      315                      320
201      Cys Asn Cys Arg Met Val His Met Pro Gly Asp Ala Pro Tyr Cys Thr
202              325                      330                      335
203      Pro Glu Gln Tyr Lys Glu Cys Ala Asp Pro Ala Leu Asp Phe Leu Val
204              340                      345                      350
205      Glu Lys Asp Gln Glu Tyr Cys Val Cys Glu Met Pro Cys Asn Leu Thr
206              355                      360                      365
207      Arg Tyr Gly Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys Ala Ser
208              370                      375                      380
209      Ala Lys Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu Gln Tyr Ile Gly
210      385                      390                      395                      400
211      Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Val Leu Asn Tyr Glu
212              405                      410                      415
213      Thr Ile Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly Leu Leu Gly Asp
214              420                      425                      430
215      Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu Thr Val
216              435                      440                      445
217      Leu Glu Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys His Arg Leu Cys
218              450                      455                      460
219      Arg Arg Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser Ser Ala Asp Lys
220      465                      470                      475                      480
221      Gly Val Ala Leu Ser Leu Asp Asp Val Lys Arg His Asn Pro Cys Glu
222              485                      490                      495
223      Ser Leu Arg Gly His Pro Ala Gly Met Thr Tyr Ala Ala Asn Ile Leu
224              500                      505                      510
225      Pro His His Pro Ala Arg Gly Thr Phe Glu Asp Phe Thr Cys
226              515                      520                      525
227      <210> SEQ ID NO 3
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229      <212> TYPE: DNA
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237      1                      5                      10                      15
238      gcc cac atc ttc tcc tac gag cgg ctg tct ctg aag cgg gca ctg tgg      96
239      Ala His Ile Phe Ser Tyr Glu Arg Leu Ser Leu Lys Arg Ala Leu Trp
240              20                      25                      30
241      gcc ctg tgc ttc ctg ggc tcg ctg gct gtg ctg ctg tgt gtg tgc acg      144
242      Ala Leu Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val Cys Thr
243              35                      40                      45
244      gag cgt gtg cag tac tac ttc cac tac cac cat gtc acc aag ctc gac      192

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION US/09/129,758

DATE: 03/15/1999

TIME: 08:37:47

Input Set: I129758.RAW

Line ? Error/Warning

Original Text

-----  
333 W Invalid/Missing Amino Acid Numbering

1300 W "N" or "Xaa" used: Feature required

1360 W "N" or "Xaa" used: Feature required

1372 W "N" or "Xaa" used: Feature required

Thr Leu Ser Xaa Glu Ile Trp Thr Tyr Leu G

ttyccngcnr tnacnntntg yaay

canarnccna nntgnccncc dawrtc